

CLAIMS:

1. An array in which different kinds of biosubstances obtained from an organism of interest, or synthetic substances interacting with such biosubstances are arranged and
5 immobilized on a support in an orderly manner,

the different kinds of biosubstances or the synthetic substances being arranged such that a chromosomal order of base sequence blocks corresponding to the biosubstances is ascertainable.

10 2. An array as set forth in claim 1, wherein at least part of the different kinds of biosubstances or the synthetic substances are arranged in the chromosomal order of the base sequence blocks corresponding to the biosubstances.

3. An array as set forth in claim 1 or 2, wherein the
15 support includes a label that indicates the chromosomal order of the base sequence blocks corresponding to the biosubstances.

4. An array as set forth in claim 1,
wherein the biosubstances or the synthetic substances immobilized on the support each include sequence position
20 information corresponding to the chromosomal order of the base sequence blocks corresponding to the biosubstances, and

wherein, in use, data is acquired and the sequence position information is read out, so as to rearrange sequences of the data in the chromosomal order.

25 5. An array as set forth in claim 1,
wherein the support comprises a collection of micro supports on which the biosubstances or the synthetic substances are individually immobilized,

wherein the micro supports each include sequence position
30 information corresponding to the chromosomal order of the base sequence blocks corresponding to the biosubstances, and

wherein sequences of acquired data are rearranged in the

chromosomal order based on the sequence position information.

6. An array as set forth in any one of claims 1 through 5, wherein the biosubstances comprise nucleic acids or polypeptides.

5 7. An array as set forth in claim 6, wherein the nucleic acid comprises DNA.

8. An array as set forth in claim 7, wherein the DNA comprises a genetic marker, genomic DNA, genomic DNA treated with a restriction enzyme, cDNA, EST, or synthetic oligoDNA.

10 9. An array as set forth in claim 7 or 8, wherein the DNA immobilized on the support is arranged based on a genetic map or physical map.

10. An array as set forth in any one of claims 7 through 9, wherein genomic DNA treated with a restriction enzyme is used
15 as target DNA.

11. An array as set forth in claim 10, wherein the target DNA is fractionated by size after the treatment with a restriction enzyme.

12. An array as set forth in any one of claims 1 through 5, wherein the polypeptides comprise proteins, fragments of protein, or oligopeptides.
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13. An array as set forth in claim 12, wherein the proteins comprise enzymes, kinase, antibodies, receptors, or proteins with SH3 region.

25 14. An array as set forth in claim 12 or 13, wherein the proteins immobilized on the support are arranged based on a genetic map or physical map.

15. An array as set forth in any one of claims 1 through 14, wherein the support or micro support comprises an inorganic substrate, an organic film, or a bead.
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16. An array as set forth in any one of claims 1 through 15, which comprises any one of a micro array, a macro array, a bead

array, and a protein chip.

17. A producing process of an array, comprising the step of
orderly arranging and immobilizing on a support different kinds
of biosubstances obtained from an organism of interest, or
5 synthetic substances interacting with such biosubstances,

said step comprising arranging and immobilizing the
biosubstances or the synthetic substances according to the order
in which genes corresponding to the biosubstances are coded for
on a chromosome of the organism.

10 18. A producing process as set forth in claim 17, wherein
the biosubstances comprise nucleic acids or polypeptides.

19. A genotype identification method, comprising
identifying a target trait-including chromosome fragment, using
the array of any one of claims 7 through 11, from hybrids
15 obtained by crossing organisms.

20. An identification method as set forth in claim 19,
wherein the organisms comprise laboratory animals and plants.

21. A gene diagnosis method for identifying human
genotypes, using the identification method of claim 20.

20 22. A screening method for screening for a target
trait-carrying variety from hybrids obtained by crossing
organisms whose characteristics are to be improved, using the
array of any one of claims 7 through 11.

23. A screening method as set forth in claim 22, wherein
25 the living organisms crossed for variety improvement comprise
laboratory animals and plants, domestic animals, or crops.

24. A screening method as set forth in claim 23, wherein
the crops comprise cereals.

25. A screening method as set forth in claim 24, wherein
30 the cereals comprise rice, wheat, corn, or barley.

26. A genotype analyzing and display system, comprising:
genotype origin detecting means for comparing (a) gene

expression level information and polymorphism information
comprehensively obtained through a hybridization analysis of
hybrid individuals with the array of any one of claims 7 through
11 with (b) genetic information of parents of the hybrid
5 individuals, and a genetic map of a species to which the hybrid
individuals belong, so as to determine whether a genotype of a
hybrid individual of interest derives from which parent; and

display information generating means for gathering a
plurality of results obtained from the genotype origin detecting
10 means and, based on the results, generating display information
used to display a plurality of genotypes altogether on a
chromosome basis, so as to determine whether individual
genotypes derives from which parent.

27. A quantitative loci analyzing system which uses the
15 array of any one of claims 7 through 11, and in which a genetic
marker of a species of interest is immobilized on the array,

said quantitative loci analyzing system comprising:

genetic marker specifying means for comparing (a)
comprehensive presence information of genes of hybrid
20 individuals, obtained by hybridizing the array with a genomic
sample obtained from the hybrid individuals of a certain hybrid
line with (b) a genetic map of a species to which the hybrid
individuals belong, and genetic marker information known in the
species, so as to specify a genetic marker that exists in the
25 hybrid line; and

quantitative loci detecting means for detecting a
quantitative locus of a phenotype of interest of the hybrid
individual, by confirming whether a phenotypic value indicative
of the phenotype is linked to the genetic marker.

30 28. A gene interaction analyzing system which uses the
array of any one of claims 7 through 11, and in which a genetic
marker of a species of interest is immobilized on the array,

said gene interaction analyzing system comprising:

genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing the array with a genomic sample obtained from the hybrid individuals of a certain hybrid line (b) with a genetic map of species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line;

spot marker information generating means for comparing the specified genetic marker with the genetic marker immobilized on the support, so as to generate spot marker information, being genetic marker information for use in analysis, from hybridization results obtained from individual spots on the array; and

hereditary factor specifying means for specifying, with regard to an arbitrarily selected phenotype and gene to be analyzed, a hereditary factor of the selected phenotype by determining whether the phenotypic value indicative of the phenotype, and an expressed gene included in expression profile information obtained from the hybrid individual are linked to a plurality of spot marker information.

29. A genotype analyzing and display system, comprising:

genotype origin detecting means for comparing (a) gene expression level information and polymorphism information comprehensively obtained through a hybridization analysis of hybrid individuals using a nucleic acid array with (b) genetic information of parents of the hybrid individuals, and a genetic map of species to which the hybrid individuals belong, so as to determine whether a genotype of a hybrid individual of interest derives from which parent; and

display information generating means for gathering a

plurality of results obtained from the genotype origin detecting means and, based on the results, generating display information used to display a plurality of genotypes altogether on a chromosome basis, so as to determine whether individual
5 genotypes derives from which parent.

30. A genotype analyzing and display system as set forth in claim 29, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such
10 that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

31. A genotype analyzing and display system as set forth in claim 29 or 30, further comprising genetic map constructing means for constructing, based on genetic map constructing
15 information, a genetic map of a species to which the hybrid individuals belong.

32. A genotype analyzing and display system as set forth in claim 31, wherein the genetic map constructing information comprises names of genes and/or genetic markers known in the
20 species, and chromosomal loci of the genes and/or genetic markers.

33. A genotype analyzing and display system as set forth in any one of claims 29 through 32, wherein the genotype origin detecting means determines a genotype as being homozygous for
25 one of the parents, heterozygous, or unrecognizable to yield a result.

34. A genotype analyzing and display system as set forth in any one of claims 29 through 32, wherein the genotype origin detecting means uses genotype information and/or gene
30 expression profile information of parents as genetic information of parents.

35. A genotype analyzing and display system as set forth in

any one of claims 29 through 34, wherein the display information generating means generates display information including at least one of recombination number and recombination frequency of individual chromosomes.

5 36. A genotype analyzing and display system as set forth in any one of claims 29 through 35, wherein the display information generating means generates display information such that an origin of a genotype is identifiable based on different display colors or patterns.

10 37. A genotype analyzing and display system as set forth in any one of claims 29 through 36, comprising at least one of input means and output means.

 38. A genotype analyzing and display system as set forth in claim 37, wherein the input means receives at least one of
15 comprehensive expression level information of genes of the hybrid individuals, and genetic information of parents.

 39. A genotype analyzing and display system as set forth in claim 38, wherein the input means receives genetic map constructing information.

20 40. A genotype analyzing and display system as set forth in any one of claims 37 through 39, comprising:

 image reading means, provided as the input means, for enabling a hybridization result of the nucleic acid array to be read out as image information; and

25 image information processing means for analyzing an expression level of gene based on the image information and generating comprehensive expression level information of gene.

 41. A genotype analyzing and display system as set forth in any one of claims 37 through 40, comprising manual input
30 means, provided as the input means, for modifying at least one of: the comprehensive expression level information of gene of the hybrid individuals; the genetic information of parents; and the

genetic map constructing information.

42. A genotype analyzing and display system as set forth in any one of claims 37 through 41, wherein the output means comprises at least one of: image display means for displaying the display information on a screen; and printing means for printing the display information.

43. A genotype analyzing and display system as set forth in any one of claims 37 through 41, wherein the input means and the output means comprise external information input-output means for sending and receiving information to and from an external device.

44. A genotype analyzing and display system as set forth in any one of claims 29 through 43, wherein the nucleic acid array comprises a DNA array on which DNA is immobilized.

45. A genotype analyzing and display system as set forth in claim 44, wherein the DNA immobilized on the DNA array comprises a genetic marker, genomic DNA, genomic DNA treated with a restriction enzyme, cDNA, EST, or synthetic oligoDNA.

46. A genotype analyzing and display system as set forth in any one of claims 29 through 45, which comprises any one of a micro array, a macro array, and a bead array.

47. A genotype identification method, comprising identifying a target trait-including chromosome fragment, using the genotype analyzing and display system of any one of claims 29 through 46, from hybrids obtained by crossing organisms.

48. An identification method as set forth in claim 47, wherein the organisms comprise laboratory animals and plants.

49. A screening method for screening for a target trait-carrying variety from hybrids obtained by crossing organisms whose characteristics are to be improved, using the genotype analyzing and display system of any one of claims 29 through 46.

50. A screening method as set forth in claim 49, wherein the organisms crossed for variety improvement comprise laboratory animals and plants, domestic animals, or crops.

- 5 51. A quantitative loci analyzing system, comprising:
genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing a genomic sample of the hybrid individuals of a certain hybrid line with a nucleic acid
10 array on which a genetic marker of a species of interest is immobilized with (b) a genetic map of a species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line; and
15 quantitative loci detecting means for detecting a quantitative locus of a phenotype of interest of the hybrid individual, by confirming whether a phenotypic value indicative of the phenotype is linked to the genetic marker.

- 20 52. A quantitative loci analyzing system as set forth in claim 51, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

- 25 53. A quantitative loci analyzing system as set forth in claim 51 or 52, further comprising genetic map constructing means for constructing, based on genetic map constructing information, a genetic map of a species to which the hybrid individuals belong.

- 30 54. A quantitative loci analyzing system as set forth in claim 53, wherein the genetic map constructing information comprises names of genes and/or genetic markers known in the

species, and chromosomal loci of the genes and/or genetic markers.

55. A quantitative loci analyzing system as set forth in any one of claims 51 through 54, wherein the genetic marker
5 information used by the genetic marker specifying means comprises a genetic marker with polymorphism.

56. A quantitative loci analyzing system as set forth in claim 55, wherein the genetic marker comprises SNP or RFLP.

57. A quantitative loci analyzing system as set forth in any one
10 of claims 51 through 56, wherein the quantitative loci detecting means detects a quantitative locus of phenotype by interval mapping.

58. A quantitative loci analyzing system as set forth in any one of claims 51 through 57, comprising:

15 image reading means for enabling a hybridization result of the nucleic acid array to be read out as image information; and
image information processing means for analyzing the image information and generating comprehensive expression level information of gene.

20 59. A quantitative loci analyzing system as set forth in any one of claims 51 through 57, comprising at least one of input means and output means.

60. A quantitative loci analyzing system as set forth in claim 59, wherein the input means receives at least one of the
25 genetic marker information and the phenotypic value.

61. A quantitative loci analyzing system as set forth in claim 60, wherein the input means receives at least one of the genetic map and the genetic map constructing information.

62. A quantitative loci analyzing system as set forth in any
30 one of claims 59 through 61, comprising manual input means, provided as the input means, for modifying at least one of: the comprehensive presence information of gene of the hybrid

individuals; the genetic marker information, and the genetic map constructing information.

63. A quantitative loci analyzing system as set forth in any one of claims 59 through 62, wherein the output means
5 comprises at least one of image display means for displaying an analysis result on a screen; and printing means for printing an analysis result.

64. A quantitative loci analyzing system as set forth in any one of claims 59 through 63, wherein the input means and the
10 output means comprise external information input-output means for sending and receiving information to and from an external device.

65. A quantitative loci analyzing system as set forth in any one of claims 51 through 64, wherein the nucleic acid array
15 comprises a DNA array on which DNA is immobilized.

66. A quantitative loci analyzing system as set forth in any one of claims 51 through 65, wherein the nucleic acid array comprises a micro array, a macro array, or a bead array.

67. A quantitative trait analyzing method for analyzing a
20 quantitative trait of an organism, using the quantitative loci analyzing system of any one of claims 51 through 66.

68. A gene searching method for searching for a gene associated with expression of a trait of interest, using the quantitative loci analyzing system of any one of claims 51
25 through 66.

69. A variety improvement method for organisms, which uses the quantitative loci analyzing system of any one of claims 51 through 66.

70. A variety improvement method as set forth in claim 69,
30 wherein the organisms comprise laboratory animals and plants, domestic animals, or crops.

71. A gene interaction analyzing system, comprising:

genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing a genomic sample of the hybrid individuals of a certain hybrid line with a nucleic acid array on which a genetic marker of a species of interest is immobilized with (b) a genetic map of a species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line;

spot marker information generating means for comparing the specified genetic marker with the genetic marker immobilized on the nucleic acid array, so as to generate spot marker information, being genetic marker information for use in analysis, from hybridization results obtained from individual spots on the nucleic acid array; and

hereditary factor specifying means for specifying, with regard to an arbitrarily selected phenotype and gene to be analyzed, a hereditary factor of the selected phenotype by determining whether the phenotypic value indicative of the phenotype, and an expressed gene included in expression profile information obtained from the hybrid individual are linked to a plurality of spot marker information.

72. A gene interaction analyzing system as set forth in claim 70, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

73. A gene interaction analyzing system as set forth in claim 71 or 72, further comprising genetic map constructing means for constructing, based on genetic map constructing information, a genetic map of a species to which the hybrid

individuals belong.

74. A gene interaction analyzing system as set forth in claim 73, wherein the genetic map constructing information comprises names of genes and/or genetic markers known in the species, and chromosomal loci of the genes and/or genetic markers.

75. A gene interaction analyzing system as set forth in any one of claims 71 through 74, wherein the genetic marker information used by the genetic marker specifying means comprises a genetic marker with polymorphism.

76. A gene interaction analyzing system as set forth in claim 75, wherein the genetic marker comprises SNP or RFLP.

77. A gene interaction analyzing system as set forth in any one of claims 71 through 76, wherein the spot marker information generating means generates spot marker information only for a genetic marker spot found by hybridization.

78. A gene interaction analyzing system as set forth in claim 77, wherein the spot marker information generating means generates spot marker information by including position information of a genetic marker immobilized on the nucleic acid array.

79. A gene interaction analyzing system as set forth in any one of claims 71 through 78, comprising expression profile information generating means for analyzing an expression profile in regard to a comprehensive gene expression level obtained from the hybrid individual, so as to generate expression profile information of the hybrid individual.

80. A gene interaction analyzing system as set forth in claim 79, wherein the expression profile information generating means generates expression profile information of the hybrid individual by comprehensively measuring gene expression, using

at least one of a micro array, a macro array, a bead array, and a differential display.

81. A gene interaction analyzing system as set forth in claim 80, wherein the expression profile information generating
5 means generates expression profile information using a nucleic acid array used to obtain comprehensive presence information of gene of the hybrid individual, or a nucleic acid array on which the same sample has been spotted.

82. A gene interaction analyzing system as set forth in any
10 one of claims 71 through 81, wherein the nucleic acid array comprises a DNA array on which DNA is immobilized.

83. A gene interaction analyzing system as set forth in any one of claims 71 through 82, wherein the nucleic acid array comprises a micro array, a macro array, or a bead array.

15 84. A gene interaction analyzing system as set forth in any one of claims 71 through 83, wherein the hereditary factor specifying means specifies a hereditary factor of a phenotype based on a quantitative trait locus (QTL) that exists among genetic markers obtained by interval mapping.

20 85. A gene interaction analyzing system as set forth in claim 84, wherein the hereditary factor specifying means uses information of expression level of a gene associated with the genetic marker, so as to specify a hereditary factor of the phenotype.

25 86. A gene interaction analyzing system as set forth in any one of claims 71 through 85, comprising at least one of input means and output means.

87. A gene interaction analyzing system as set forth in claim 86, wherein the input means receives at least one of:
30 comprehensive presence information of gene of the hybrid individual; the genetic marker information; the phenotypic value; and the expression profile information.

88. A gene interaction analyzing system as set forth in claim 87, wherein the input means receives at least one of the genetic map and the genetic map constructing information.

89. A gene interaction analyzing system as set forth in
5 any one of claims 86 through 88, comprising:

image reading means, provided as the input means, for enabling a hybridization result of the nucleic acid array to be read out as image information; and

10 image information processing means for analyzing an expression level of gene based on the image information and generating comprehensive expression level information of gene.

90. A gene interaction analyzing system as set forth in claim 89, wherein the input means receiving the expression profile information comprises image information reading means.

15 91. A gene interaction analyzing system as set forth in any one of claims 86 through 90, comprising manual input means, provided as the input means, for modifying at least one of: the comprehensive presence information of gene of the hybrid individuals; the genetic marker information, and the genetic map
20 constructing information.

92. A gene interaction analyzing system as set forth in any one of claims 86 through 91, wherein the output means comprises at least one of image display means for displaying an analysis result on a screen; and printing means for printing an
25 analysis result.

93. A gene interaction analyzing system as set forth in any one of claims 86 through 92, wherein the input means and the output means comprise external information input-output means for sending and receiving information to and from an
30 external device.

94. A gene interaction analyzing method for analyzing interaction between genes, using the gene interaction analyzing

system of any one of claims 71 through 93.

95. A gene searching method for searching for a gene associated with a trait of interest, using the gene interaction analyzing system of any one of claims 71 through 93.

5 96. A variety improvement method for organisms, which uses the gene interaction analyzing system of any one of claims 71 through 93.

97. A variety improvement method as set forth in claim 96, wherein the organisms comprise laboratory animals and plants,
10 domestic animals, or crops.